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Stable gene transformation in cowpea (*Vigna unguiculata* L. Walp.) using particle gun method

J. Ikea1,2*, I. Ingelbrecht2, A. Uwaifo1 and G. Thottappilly2,λ

1Biochemistry Department, University of Ibadan, Ibadan, Nigeria
2International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria

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We investigated the possibility of transforming and obtaining transgenic cowpea (*Vigna unguiculata* L Walp) plants using the particle bombardment process. Meristematic explants that could give rise to whole fertile plants were used in transformation experiments with reporter and selectable marker genes driven by a 35S CaMV promoter. Conditions for optimal delivery of DNA to explants were established based on transient gus expression assays two days after bombardment. The size of microcarriers, microflight distance and helium pressure significantly affected transient expression of reporter genes. A total of 1692 explants were bombarded with DNA-coated particles and placed on 3 mg/l bialaphos selective medium. Only 12 regenerated shoots produced seeds eventually, and all were GUS negative even though 7 gave positive PCR signals with the bar primer. Eight out of 1400 seeds from T₀ plants were GUS positive. DNA from eight of the GUS positive seedlings were amplified with both the gus and bar primers in PCR analysis but only two gave a positive Southern signal. Only two of the 3557 T₂ seedlings obtained were GUS positive. However, 3 seedlings survived Basta spray. The two GUS positive and 3 Basta surviving seedlings gave positive Southern hybridisation signals. Twelve T₃ seedlings from these were GUS positive and also gave positive Southern hybridisation signals. The positive reaction of T₁, T₂ and T₃ seedlings under Southern analysis confirms the stable integration of introduced genes and the transfer of such genes to progenies. However, the level of expression of introduced genes in cowpea cells is very low and this accounted for the high mortality rate of progenies under Basta spray.

Key words: Transformation, particle bombardment, gus assay, transient expression, reporter gene, basta, bar gene.

INTRODUCTION

Transformation of many plant species has become routine, permitting the introduction of characteristics that would not be possible by conventional breeding. Most legume transformation studies have used *Agrobacterium tumefaciens* to generate for example transgenic soya bean (Hinchee et al., 1994), chickpeas (Fontana et al., 1993), peas (Puouti-Kaerlas et al., 1990; Schroeder et al., 1993; Grant et al., 1995) and cowpea (Muthukumar et al., 1996; Kononowicz et al., 1993, 1997). Particle bombardment has also been used to produce transgenic soybean (McCabe et al., 1988), beans (Russell et al., 1993), peanut (Brar et al., 1994) and alfalfa (Pereira and Erickson, 1995). Stable integration and expression of transgenes in progeny of cowpeas using particle bombardment has not been reported. Various explants of *V. unguiculata* have been used in experiments with *Agrobacterium* or direct DNA transfer methods but the main obstacle has been difficulties in regeneration. Mature embryos (Penza et al., 1991; Akella and Lerquin 1993), leaf discs (Garcia et al., 1986, 1987) and cotyledons (Muthukumar et al., 1996; Kononowicz et al., 1997) have been used. Neither Garcia and co-workers (1986, 1987) nor Penza and co-workers (1991) were able to recover plants from transformed tissues.
Transformation of cotyledon explants of cowpea was performed using *Agrobacterium* (Muthukumar et al., 1996). Mature de-embryonated cotyledons with intact proximal ends were inoculated with *Agrobacterium tumefaciens* and cultured on a medium supplemented with 6-benzylaminopurine (BAP). Regenerated shoots selected on hygromycin were confirmed to be transgenic by Southern blot hybridisation. Chowrira et al. (1995) also reported transient expression, stable integration and expression of transgenes in the tissues and progeny of leguminous plants (including cowpea), after electroporation of DNA into intact nodal meristems. The *ptjk 142* plasmid contains the *uid A* gene under control of the CaMV 35S promoter. For microprojectile bombardment, the plasmid *ptjk 142* was used.

Particle bombardment of Primary Explants

Thirty embryonic axes maintained on Cp3 medium for 1 or 2 days after detachment were arranged in a circle of about 3 cm diameter in the centre of agar petri plates. Bombardment was carried out with a Biolistic PDS-100/He particle delivery system (*Bio-Rad*). All bombardments were performed at a pressure of 1100 psi, a 6 cm particle travel distance, an 11 mm gap distance (between the rupture disk and the macrocarrier), an 11 mm macrocarrier flying distance and a vacuum of 28 Hg inch.

Following bombardment, the explants were cultured for 2 weeks in the dark at 26°C on Cp3 medium for shoot proliferation and elongation. Explants were subsequently plated on rooting medium Cp4 (Kononowicz et al., 1995) in light (12 hr photoperiod, 20-25 µmolm⁻²s⁻¹ cool white fluorescent illumination). Developing shoots were recultured on fresh Cp4 medium at 2 weeks intervals. Shoot regeneration was conducted under continuous selection pressure (3 mg/L Bialaphos). Shoots that survived on selection medium for 3 weeks were transferred to soil after conditioning on peat-pellets in a temperature controlled environment. Plants were grown subsequently in the screen house until pod maturity.

Analysis of *gus* expression

Transient expression of the *gus* A gene was tested by histochemical staining of the tissues 48 hr after bombardment using X-Gluc (5-bromo-4-chloro-3-indolyl-β-D-glucuronidase) as described by Jefferson et al (1987). Tissues were immersed in the *gus* A assay solution and incubated overnight at 37°C. Explants were decolourised with 2-3 rinses of absolute ethanol before counting blue spots under a low magnification laboratory microscope. The number of individual cells or cell aggregates that contained a blue precipitate was counted as expression units.

Herbicide screening and application

Seedlings were sprayed with 0.125-0.2% *Basta* (Hoechst, Brussels, Belgium) using a Hills Master Sprayer (Hills Industries, Caerphilly, UK) seven days after planting. In all cases, non-transformed controls died within 3-4 days after spraying. Survivors were scored after a week and subsequently resprayed. Only those that survived two sprays were grown to maturity in the screenhouse.

**Polymersome Chain Reaction (PCR)**

Plants that regenerated following bombardment and selection were initially analysed by PCR. Two 25-mer primers which are homologous to the *uid A* gene (51-TTG CCC AGC TAT CTG TCA CTT CAC T3-31 and 51-ATG TCA CAT CAA TGC ACT TGC TTG G-31) and two 24-mer primers homologous to the bar gene (51-GGG ACT TCA GCA GGT GGG TGT AGA-31 and 51-AAC CGC AGG AGT GGA CCG ACG ACC-31) were used. PCR amplifications of DNA were performed in 50µl volumes containing 100mM Tris-HCl (pH 9.0), 500mM KCl, 25mM MgCl₂, 1% Triton X-100, 2.5 mM of each dNTP (Promega), 250ng of primers, 2U of DNA polymerase (Promega) and 500ng genomic DNA overlaid with 30µl mineral oil.
Amplifications were performed in a Perkin Elmer-Cetus DNA cycler 480. The amplification temperature cycle for the bar gene was as follows: Preheating at 94°C for 2.5 min followed by one cycle of 1 min each at 94°C, 60°C and 72°C and 34 cycles of 30 sec each at 94°C, 60°C and 72°C. For the uid A gene, there was a preheating at 94°C for 3 min and 1 cycle of 1 min each at 94°C, 55°C and 72°C and 34 cycles of 30 sec each at 94°C, 55°C and 72°C. The programmes ended at 4°C for cooling. Products were electrophoresed in 1.5% agarose gel and visualised under UV light by ethidium bromide staining.

Southern blot analysis

The modified CTAB DNA extraction procedure for Musa and Ipomoea (Gawel and Jarret, 1991) was adopted for genomic DNA isolation. Southern blotting and hybridization were performed as previously described (Southern, 1975; Sambrook et al., 1989). Genomic DNA (10 µg) was digested with Hind III, separated on 0.8% agarose gel, blotted onto nylon membrane (Hybond N, Amersham) and cross-linked to the filter with ultraviolet radiation. Non-radioactive labelling with digoxigenin-11-dUTP and hybridisation was carried out according to the manufacturer's manual (Boehringer Mannheim).

RESULTS AND DISCUSSION

Optimization of conditions for DNA delivery

To optimize DNA delivery, conditions for particle bombardment were established based on transient expression assay using histochemical techniques (Jefferson et al., 1987; Sanford et al., 1993). Reporter gene activity was evaluated by determining the expression of chimeric gene constructs (pDPG 208 and ptjk 142) in explants. These constructs consisted of the CaMV 35S promoter–uid A coding sequence. When subjected to GUS histochemical assay, cowpea explants exhibited characteristic blue cells typical of transient expression of the uid A gene two days after DNA delivery (Figure 1). The transformed cells appeared to be randomly distributed on the surface of explants. In some cases, the entire embryonic explants were totally blue, and this could be as a result of diffusion of GUS reaction product to adjacent cells. Control explants that were not bombarded or those that were bombarded with microcarriers not coated with DNA did not exhibit any uid A expressing cells. Similar uid A expression patterns were observed for cowpea and sweet potato previously (Knonowicz et al., 1995; Prakash and Varadarajan, 1992). Based on the transient uid A expression, particle size, target distance, helium pressure, number of bombardments and vacuum significantly affected transient expression of reporter genes. These findings are very similar to those reported for cowpea and barley (Knonowicz et al., 1997; King and Kasha, 1994). The interaction between bombardment pressure and target distance showed that the higher the pressure, the longer the distance. Best results were obtained at pressure of 1100 psi, target distance of 6 cm and 28 Hg in vacuum. Bombarding the explants two times increased the number of cells giving transient gene expression and this could be due to the fact that multiple bombardments allow better coverage of the target areas and compensate for misfires from faulty and poorly set rupture discs as was the case in rice (Wang et al., 1988). By using the same range of sizes reported for maize (Klein et al., 1988), gene transfer in wheat was shown to be most efficient with microprojectiles 1.2 µm in diameter. The results obtained in optimizing different parameters are in line with those that have been obtained for other crops. Bombardment conditions chosen were those at which 70% of shoot embryos showed more than 20 blue spots per embryos hit.

Tissue Culture and Plant Regeneration

Two media, Cp3 (shoot elongation) and Cp4 (rooting) (Knonowicz et al., 1995, 1997) were used to regenerate plants. Embryonic axes used as primary target explants were obtained by excising embryos from mature seeds. Bombarded explants were cultured for two or three weeks in the dark on Cp3 medium. The culture conditions induced multiple shoots within a month from which plants ready to transfer to soil were obtained within two months when cultured in the absence of selectable agents. Similar results have been reported (Knonowicz et al, 1997). Bialaphos (3 mg/L) was used to select for transformed shoots after bombardment. Bombarded explants surviving for three weeks on bialaphos medium (Figure 2) as in Phaseolus vulgaris transformation (Russel et al., 1993) were grown up to adult plants. This concentration was very effective and eliminated the selection of many escapes. Previously for both legumes and cereals, concentrations ranging from 1-5 mg/L bialaphos have been used (Knonowicz et al., 1997; Spencer et al., 1990; Gordon-Kamm et al., 1990; Russel...
et al., 1993). Only 152 shoots survived out of a total 630 placed on the selection medium. The 152 shoots surviving selection accounts for 24% of those put on selection. Forty-eight shoots of those surviving selection (32%) were well rooted and conditioned for soil in jiffypeat pellets. At the end, twelve plants (8% of those selected) produced seeds. The rest were affected by fungal attacks. A similar case of low efficiency has been observed involving the kanamycin resistance gene in soybean (McCabe et al., 1988).

Molecular evaluation of T₀ plants

Even though the T₀ plants were all GUS negative, DNA from all 12 plants were amplified with both the bar and uid A primers (Table 1). Southern hybridisation of some of the PCR products with bar gene probe confirmed the identity of the amplified products (gel results not shown for T₀ plants). Similar confirmatory assays have been done for cowpea, banana and plantain (Kononowicz et al., 1997; Sagi et al., 1995). The amplification of DNA samples from GUS negative plants and the subsequent confirmation by Southern analysis proves that the plants were transformed with the exogenous DNA integrated into the genome. There are reports of uid A genes fused with selectable marker genes (npt-II or bar) not being expressed even though the selectable markers were expressed (Pereira and Erickson, 1995; Russel et al., 1993; Fitch et al., 1992; McCown et al., 1991).

Molecular evaluation of T₁ plants

Basta spraying, GUS assay, PCR and Southern analysis were used to evaluate all T₁ seedlings (Table 1). One thousand four hundred T₁ seedlings were raised from the twelve T₀ plants. Two hundred and thirty-nine of these were subjected to gus assay and only eight showed positive gus reaction. The GUS reactions were very strong with the midribs showing blueness. Using T₀ plants, the potential for germ-line transformation can be evaluated based on the observations of Christou and McCabe (1992). They observed that whenever any part of the vascular system of a soybean leaf produced from meristem bombardment expressed the reporter gene, it was possible to pass that gene to its progeny at very high frequency. Thus these plants have a very high chance of germ-line transformation. GUS positive plants were spared from Basta spray and only one seedling survived.
### Table 1. Molecular evaluation of T₀ plants and their T₁, T₂ and T₃ progenies.

<table>
<thead>
<tr>
<th>Assay</th>
<th>T₀ Plants</th>
<th>T₁ Plants</th>
<th>T₂ Plants</th>
<th>T₃ Plants</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Total</td>
<td>Fraction assayed</td>
<td>+ve</td>
<td>% +ve</td>
</tr>
<tr>
<td>Gus</td>
<td>12</td>
<td>12</td>
<td>None</td>
<td>0</td>
</tr>
<tr>
<td>Basta spray (0.2%)</td>
<td>ND</td>
<td>1400</td>
<td>1392</td>
<td>1</td>
</tr>
<tr>
<td>PCR Bar Primer</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>100</td>
</tr>
<tr>
<td>PCR-gus Primer</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>100</td>
</tr>
<tr>
<td>Pcr/Southern</td>
<td>12</td>
<td>7</td>
<td>7</td>
<td>100</td>
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<tr>
<td>Southern</td>
<td>ND</td>
<td>2</td>
<td>2</td>
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a = Gus positive seedlings were not sprayed with basta
nd=not done
The spray out of a total of 1392 assayed. The high mortality rate of T1, T2 and T3 plants under Basta spray does not necessarily indicate the non-integration of the bar gene or high application levels of the Basta. Plants that did not express the phosphinothricin-resistance gene in the leaf tissue but were shown to have the gene by Southern analysis have been reported for peas (Grant et al., 1995). The 0.2% of Basta applied is within the ranges reported for other crops even though different crop plants may have different responses to the herbicide (Christou et al., 1991; Gordon-Kamm et al., 1990). The most logical conclusion when plants which definitely carried the bar gene (clear PCRs and Southerns) react negatively on the leaf-painting assay or spraying with Basta will be that the level of expression is not enough to induce resistance against Basta.

DNA samples from eight GUS positive T1 plants subjected to PCR analysis were all amplified with both the bar and gus primers. Southern analysis of genomic DNA samples from two of the plants confirmed the stable integration of the bar gene (Figure 3). In any method to produce transgenic seed plants, the critical aspect is whether or not the plants can pass the introduced traits to the progeny. The chimeric T0 plants obtained were fertile and passed the traits to their progeny even though the level of expression of the bar gene seems to be very low.

**Molecular evaluation of T2 plants**

Four hundred and one (401) T2 seedlings out of a total of 3557 were subjected to GUS assay. Only two gave good positive reaction (Table 1). Seedlings that reacted negatively and all other T2 seedlings totalling 3555 were sprayed with Basta (0.2%). Three seedlings survived the herbicide spray (Figure 4). The five T2 plants that either were gus positive or survived herbicide treatment were subjected to Southern analysis. Genomic DNA from all five hybridized with bar gene probe (data not shown).

**Molecular Evaluation of T3 plants**

Five hundred and ninety-eight T3 plants were evaluated by Gus assay and Basta spraying. Twelve of these were positive and were therefore not subjected to Basta spraying. All the negative ones were sprayed with Basta (0.2%) but none survived (Table 1). All twelve positive plants were subjected to Southern analysis. The bar gene fragment was detected in the genomic DNA extracted from all twelve plants (data not shown).
The positive reactions under PCR and Southern analyses of genomic DNA samples from T1, T2, and T3 plants confirm the transfer of the bar gene up to the third generation. The bar gene was detected in 5 T2 and 12 T3 plants. Despite the low level expression of the bar gene under Basta spray, three T2 plants were able to survive almost unaffected by Basta. Two T2 and twelve T3 plants were also gus positive. All T2 and T3 plants that were gus positive and resistant to Basta (0.2%) were also positive in Southern analysis using the bar probe. To obtain transformant T1 progeny, the L2 layer of the meristem is normally the target for the DNA coated particles (Christou, 1992; Christou et al., 1993), since this layer gives rise to the germine cells that produce sperm and egg (Sussex, 1989; Irish, 1991; Szymkowiak and Sussex, 1992). An earlier report on developing a transformation system for cowpea (Knonowicz et al., 1997), only confirmed the integration of the bar gene into the genome of T2 plants. No transformed T1 progeny was obtained from transgenic chimeras. Thus this work is the first report of generation of transgenic cowpea by particle bombardment with molecular evidence of stable integration of introduced gene in T1, T2 and T3 progenies.

REFERENCES


